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=> dis his full

     (FILE 'HOME' ENTERED AT 09:20:35 ON 15 AUG 2007)

     FILE 'CAPLUS, MEDLINE, EMBASE, BIOSIS, SCISEARCH' ENTERED AT 09:21:18 ON
     15 AUG 2007
L1           112 SEA ABB=ON  PLU=ON  QIN NING/AU
L2            11 SEA ABB=ON  PLU=ON  CODD ELLEN/AU
L3            11 DUP REM L2 (0 DUPLICATES REMOVED)
                 DIS L3 1-11 TI SO
L4             2 SEA ABB=ON  PLU=ON  "ALPHA2 DELTA CALCIUM CHANNEL SUBUNIT"
L5             2 DUP REM L4 (0 DUPLICATES REMOVED)
                 DIS L5 1-2 IBIB ABS
L6             2 SEA ABB=ON  PLU=ON  "ALPHA DELTA CALCIUM CHANNEL"
L7          1094 SEA ABB=ON  PLU=ON  ALPHA (S) DELTA (S) CALCIUM (S) CHANNEL
L8         19254 SEA ABB=ON  PLU=ON  GABAPENTIN OR NEURONTIN
L9           373 SEA ABB=ON  PLU=ON  L7 AND L8
L10          303 SEA ABB=ON  PLU=ON  L7 (P) L8
L11          191 SEA ABB=ON  PLU=ON  L7 (S) L8
L12           67 SEA ABB=ON  PLU=ON  L11 AND HUMAN
L13           46 DUP REM L12 (21 DUPLICATES REMOVED)
                 DIS L13 20-46 TI SO AU
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EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	19	Qin adj Ning	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2007/08/15 09:10
L2	52	Codd adj Ellen	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2007/08/15 09:11
L3	705	"voltage gated calcium channel"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2007/08/15 09:12
L4	83	"alpha 2 delta subunit"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2007/08/15 09:13
L5	22	l3 and l4	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2007/08/15 09:15
L6	1	"alpha 2 delta 4 subunit"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2007/08/15 09:16
L7	0	"alpha 2 delta 4 calcium channel"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2007/08/15 09:17
L8	6	"alpha2 delta4 calcium channel"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2007/08/15 09:17

Seq ID # 10

<!--StartFragment-->RESULT 3
AAY92321
ID AAY92321 standard; protein; 1120 AA.
XX
AC AAY92321;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human alpha-2-delta-D calcium channel subunit.
XX
KW alpha-2-delta-D; calcium channel subunit; 3p21.1; gabapentin; cytostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant.
XX
OS Homo sapiens.
XX
PN WO200020450-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US023519.
XX
PR 07-OCT-1998; 98US-0103322P.
PR 30-OCT-1998; 98US-0106473P.
PR 29-DEC-1998; 98US-0114088P.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Moldover B, Offord JD;
XX
DR WPI; 2000-303744/26.
DR N-PSDB; AAA09254.
XX
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer.
XX
PS Claim 8; Page 67; 88pp; English.
XX
CC The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC sleep interference, anxiety, amyotropic lateral sclerosis (ALS), multiple
CC sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC syndromes, mood, depression or cancer
XX
SQ Sequence 1120 AA;

  Query Match   94.1%; Score 5386.5; DB 3; Length 1120;
  Best Local Similarity   98.0%; Pred. No. 0;
  Matches 1033; Conservative   5; Mismatches   13; Indels   3; Gaps   2;

Qy   11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
               :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

60

problem

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Qy        71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy       131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy       191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy       251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
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Db       298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy       311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
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Db       358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy       371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
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Db       418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy       431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy       491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
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Db       538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy       551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy       611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy       671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy       731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy       791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
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Qy       851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1030
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Qy       1031 DSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
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Db       1078 DSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1110

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Seq ID #9
nucleicacid

<!--StartFragment-->RESULT 3
AAA09254
ID AAA09254 standard; cDNA; 5073 BP.
XX
AC AAA09254;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human alpha-2-delta-D gene.
XX
KW alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   3. .3365
FT   /*tag= a
XX
PN WO200020450-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US023519.
XX
PR 07-OCT-1998; 98US-0103322P.
PR 30-OCT-1998; 98US-0106473P.
PR 29-DEC-1998; 98US-0114088P.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Moldover B, Offord JD;
XX
DR WPI; 2000-303744/26.
DR P-PSDB; AAY92321.
XX
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer.
XX
PS Claim 1; Page 64-66; 88pp; English.
XX
CC The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC sleep interference, anxiety, amyotropic lateral sclerosis (ALS), multiple
CC sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC syndromes, mood, depression or cancer
XX
SQ Sequence 5073 BP; 1280 A; 1390 C; 1347 G; 1056 T; 0 U; 0 Other;

  Query Match   88.5%; Score 3085.6; DB 3; Length 5073;
  Best Local Similarity   98.8%; Pred. No. 0;
  Matches 3109; Conservative   0; Mismatches   39; Indels   0; Gaps   0;

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Qy        219 GGACAGAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAA 278
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Db        173 GGAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAA 232

Qy        279 ATACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGAT 338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGAT 292

Qy        339 CGAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCT 398
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Db        293 CGAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCT 352

Qy        399 GCGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAA 458
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Db        353 GCGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAA 412

Qy        459 CCACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAG 518
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Db        413 CCACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAG 472

Qy        519 GGACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCA 578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 GGACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCA 532

Qy        579 CTTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTA 638
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Qy        639 CAACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTT 698
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Qy        699 CGTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGG 758
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Db        653 CGTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGG 712

Qy        759 ATTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTT 818
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Db        713 ATTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTT 772

Qy        819 TGACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGAT 878
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Db        773 TGACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGAT 832

Qy        879 TTTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCAT 938
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Qy        939 CACCACCATCTTGGACACCCTGGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGA 998
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Qy        999 CTACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAA 1058
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Qy       1059 TCGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGGTCGTGGA 1118
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Db       1013 TCGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGGTCGTGGA 1072

Qy       1119 CCAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAG 1178
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Db       1073 CCAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAG 1132

Qy       1179 CCTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGT 1238
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Db       1133 CCTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGT 1192

Qy       1239 GTTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAG 1298
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Db       1253 AGAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACAC 1312

Qy       1359 GCAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAG 1418
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Qy       1419 CCGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAG 1478
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Qy       1539 CTTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGA 1598
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Qy       1599 TGTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATA 1658
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Db       1553 TGTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATA 1612

Qy       1659 CGCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTA 1718
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Db       1613 CGCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTA 1672

Qy       1719 CAGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGT 1778
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Db       1673 CAGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGT 1732

Qy       1779 GGAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTAC 1838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1733 GGAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTAC 1792

Qy       1839 TCTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAA 1898
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Db       1793 TCTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAA 1852

Qy       1899 TGACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGCGGTGCTGTCCCG 1958
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Db       1853 TGACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCG 1912

Qy       1959 GGGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTT 2018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1913 GGGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTT 1972

Qy       2019 GCTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCC 2078
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Db       1973 GCTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCC 2032

Qy       2079 AGACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCC 2138
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Db       2033 AGACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCC 2092

Qy       2139 AGACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGC 2198
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Qy       2199 CCCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGT 2258
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Qy       2259 GGTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGG 2318
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Db       2213 GGTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGG 2272

Qy       2319 CTCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCAC 2378
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Db       2273 CTCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCAC 2332

Qy       2379 CCTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGT 2438
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Db       2333 CCTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGT 2392

Qy       2439 CTTCAACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGC 2498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2393 CTTCAACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGC 2452

Qy       2499 AAGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGT 2558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2453 AAGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGT 2512

Qy       2559 CCAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCAC 2618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2513 CCAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCAC 2572

Qy       2619 TGTGGATGGGCCGTACACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGA 2678
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       2573 TGTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGA 2632

Qy       2679 CAACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGA 2738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2739 GGTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTAT 2798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2799 GTATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCT 2858
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Qy       2859 GGTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCT 2918
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Qy       2919 GTTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAG 2978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2873 GTTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAG 2932
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Qy       2979 TGTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGA 3038
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Qy       3039 GTACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGG 3098
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Qy       3099 GCCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGT 3158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3159 GACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGT 3218
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Qy       3219 CAAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACC 3278
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Qy       3279 AGACTCCTGCCACGCCTTCCATCCAGAGGTGCGGGTTGAGGCGGATCGAGGGTGGGCTGG 3338
              |||||||||||||||||||||||||||| |   |   |||      | ||     | |
Db       3233 AGACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGGCGCCTCGGA 3292

Qy       3339 ATTTTCATCCCCAAACCCTCTGTGCCTG 3366
                  ||| || |    || ||   ||||
Db       3293 CACCTCAGCCTCGCCGCCCCTACTCCTG 3320
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